

M-T Am DAVIS

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/583,848

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TIME: 16:15:42

INPUT SET: S37021.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

20

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
van der Bruggen, Pierre; Boon-Falleur, Thierry

(ii) TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

(iii) NUMBER OF SEQUENCES: 30

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Felfe & Lynch
(B) STREET: 805 Third Avenue
(C) CITY: New York City
(D) STATE: New York
(F) ZIP: 10022

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
(B) COMPUTER: IBM
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/583,848
(B) FILING DATE: 31-MAY-2000
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:US/09/404,026
(B) FILING DATE: 23-SEPT-1999

ENTERED

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:US/08/037,230
(B) FILING DATE: 26-MARCH-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US92/04354
(B) FILING DATE: 22-MAY-1992

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/807,043

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47 (B) FILING DATE: 12-DECEMBER-1991
48
49 (ix) PRIOR APPLICATION DATA:
50 (A) APPLICATION NUMBER: 07/764,364
51 (B) FILING DATE: 23-SEPTEMBER-1991
52
53 (x) PRIOR APPLICATION DATA:
54 (A) APPLICATION NUMBER: 07/728,838
55 (B) FILING DATE: 9-JULY-1991
56
57 (xi) PRIOR APPLICATION DATA:
58 (A) APPLICATION NUMBER: 07/705,702
59 (B) FILING DATE: 23-MAY-1991
60
61 (xii) ATTORNEY/AGENT INFORMATION:
62 (A) NAME: Hanson, Norman D.
63 (B) REGISTRATION NUMBER: 30,946
64 (C) REFERENCE/DOCKET NUMBER: LUD 5353
65
66 (xiii) TELECOMMUNICATION INFORMATION:
67 (A) TELEPHONE: (212) 688-9200
68 (B) TELEFAX: (212) 838-3884
69
70
71
72 (2) INFORMATION FOR SEQ ID NO: 1:
73 (i) SEQUENCE CHARACTERISTICS:
74 (A) LENGTH: 462 base pairs
75 (B) TYPE: nucleic acid
76 (C) STRANDEDNESS: single
77 (D) TOPOLOGY: linear
78 (ii) MOLECULE TYPE: genomic DNA
79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
80
81
82
83 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60
84 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT 120
85 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCGCCT ACAGCTCTAG 180
86 CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240
87 CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
88 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG CATGCATTGT 360
89 GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT 420
90 TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC 462
91
92
93
94 (2) INFORMATION FOR SEQ ID NO: 2:
95 (i) SEQUENCE CHARACTERISTICS:
96 (A) LENGTH: 675 base pairs
97 (B) TYPE: nucleic acid
98 (C) STRANDEDNESS: single
99 (D) TOPOLOGY: linear

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100      (ii) MOLECULE TYPE:  genomic DNA
101      (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 2:
102
103
104      ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT      48
105      Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
106                      5                      10                      15
107      GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA      96
108      Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
109                      20                      25                      30
110      GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA      144
111      Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
112                      35                      40                      45
113      AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG      192
114      Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
115                      50                      55                      60
116      TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC      240
117      Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
118                      65                      70                      75                      80
119      TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC      288
120      Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
121                      85                      90                      95
122      GAC GAC GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT      336
123      Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
124                      100                     105                     110
125      GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG      384
126      Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
127                      115                     120                     125
128      GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG      432
129      Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
130                      130                     135                     140
131      GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG      480
132      Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
133                      145                     150                     155                     160
134      AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC      528
135      Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
136                      165                     170                     175
137      CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT      576
138      Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
139                      180                     185                     190
140      GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG      624
141      Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
142                      195                     200                     210
143      GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT      672
144      Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
145      220                      225                      230                      235
146
147      TAG      675
148
149
150
151
152      (2) INFORMATION FOR SEQ ID NO: 3:

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153 (i) SEQUENCE CHARACTERISTICS:
154 (A) LENGTH: 228 base pairs
155 (B) TYPE: nucleic acid
156 (C) STRANDEDNESS: single
157 (D) TOPOLOGY: linear
158 (ii) MOLECULE TYPE: genomic DNA
159 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
160
161
162 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT, 60
163 TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT 120
164 TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC 180
165 ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC 228
166
167
168 (2) INFORMATION FOR SEQ ID NO: 4:
169 (i) SEQUENCE CHARACTERISTICS:
170 (A) LENGTH: 1365 base pairs
171 (B) TYPE: nucleic acid
172 (C) STRANDEDNESS: single
173 (D) TOPOLOGY: linear
174 (ii) MOLECULE TYPE: genomic DNA
175 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
176
177
178 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50
179 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100
180 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
181 AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCCTT 200
182 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
183 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
184 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG 350
185 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
186 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
187 ACCCTTTGTG CC 462
188 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
189 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
190 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
191 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
192 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
193 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
194 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756
195 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
196 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAT GAA TCA GAA 840
197 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
198 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT 924
199 GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT 966
200 TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG 1008
201 AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT 1050
202 GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG 1092
203 GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 1134
204 TAG 1137
205 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG 1187

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206	TTGTTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA	1237
207	ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT	1287
208	CTGACTGCAT GGTGAACCTT CATATGATAC ATAGGATTAC ACTTGTACCT	1337
209	GTTAAAAATA AAAGTTTGAC TTGCATAC	1365
210		
211		
212		
213	(2) INFORMATION FOR SEQ ID NO: 5:	
214	(i) SEQUENCE CHARACTERISTICS:	
215	(A) LENGTH: 4698 base pairs	
216	(B) TYPE: nucleic acid	
217	(C) STRANDEDNESS: single	
218	(D) TOPOLOGY: linear	
219	(ii) MOLECULE TYPE: genomic DNA	
220	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
221		
222		
223	ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
224	GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT	100
225	CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG	150
226	AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT	200
227	CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA	250
228	CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
229	AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCTTTT GCTCTCCAG	350
230	CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG	400
231	CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	450
232	ACCCTTTGTG CC	462
233	ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA	504
234	GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
235	TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
236	TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
237	ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
238	TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
239	GAT GAA GAC GAT GAG GAT GAT GAT GAC TAC TAC GAC GAC	756
240	GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
241	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
242	GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
243	GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T	916
244	GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA	966
245	CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC	1016
246	TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC	1066
247	CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC	1116
248	TTCACTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC	1166
249	TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC	1216
250	TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AACCCCTCCCC TTCCTGTTCC	1266
251	CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT	1316
252	TCACCAGCTT TGCTCTCCCT GCTCCCCTCC CCCTTTTGCA CCTTTTCTTT	1366
253	TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT	1416
254	CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG	1466
255	TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT	1516
256	CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT	1566
257	TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GTCCTGGCAC	1616
258	TCACTCTGTA GACCAGGCTG GCCTCAAAC CAGAAATCTG CCTGCCTCTG	1666

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SEQUENCE VERIFICATION REPORT
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SEQUENCE MISSING ITEM REPORT
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COUNTRY

PRIOR APPLICATION DATA More Identifiers Found Than MAX Allowed

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SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/583,848

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